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DATE: 05/07/2002 RAW SEQUENCE LISTING TIME: 11:16:47 PATENT APPLICATION: US/10/040,647

Input Set : N:\Crf3\RULE60\10040647.raw Output Set: N:\CRF3\05072002\J040647.raw

			SEQUENCE LISTING
			RAL INFORMATION:
	5		APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David
	7	, ,	TITLE OF INVENTION: NOVEL MOLECULES
	9	, ,	NUMBER OF SEQUENCES: 30
	11	(iv)	CORRESPONDENCE ADDRESS:
	12		(A) ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
	13		(B) STREET: 400 GARDEN CITY PLAZA
	14		(C) CITY: GARDEN CITY
	15		(D) STATE: NEW YORK (E) COUNTRY: USA (F) ZIP: 11530
	16		(E) COUNTRY: USA
	17		(F) ZIP: 11530
	19	(∀)	COMPUTER READABLE FORM:
	20		(A) MEDIUM TYPE: Floppy disk
	21		(B) COMPUTER: IBM PC compatible
	22		(C) OPERATING SYSTEM: PC-DOS/MS-DOS
	23		(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
_	25	(V1)	CURRENT APPLICATION DATA:
>			(A) APPLICATION NUMBER: US/10/040,647
>			(B) FILING DATE: 07-Jan-2002
	28		(C) CLASSIFICATION:
	42	(V11)	PRIOR APPLICATION DATA:
	31		(A) APPLICATION NUMBER: 09/023,942
	32		(B) FILING DATE:
	36		(A) APPLICATION NUMBER: PO5101/97
	37 40		(B) FILING DATE: 13-FEB-1997
	41		(A) APPLICATION NUMBER: PP0422/97 (B) FILING DATE: 18-NOV-1997
	43		(A) APPLICATION NUMBER: International PCT Application
	44		(B) FILING DATE: 13-FEB-1998
	44	/rri i i \	ATTORNEY/AGENT INFORMATION:
	47	(^ TTT)	(A) NAME: DIGIGLIO, FRANK S
	48		(B) REGISTRATION NUMBER: 31,346
	49		(C) REFERENCE/DOCKET NUMBER: 11168
	51		TELECOMMUNICATION INFORMATION:
	52	(IX)	(A) TELEPHONE: (516) 742 4343
	53		(B) TELEFAX: (516) 742 4366
	54		(C) TELEX: 230 901 SANS UR
		(2) INFO	RMATION FOR SEQ ID NO: 1:
	60	• •	SEQUENCE CHARACTERISTICS:
	61	(1)	(A) LENGTH: 32 base pairs
	62		(B) TYPE: nucleic acid
	63		(C) STRANDEDNESS: single
	0.0		(C) Dilumbaniable Dingre

C-C-

32

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```
64
                   (D) TOPOLOGY: linear
            (ii) MOLECULE TYPE: DNA
W--> 66
            (ix) FEATURE:
     68
                   (A) NAME/KEY: modified base
     69
                   (B) LOCATION: 15
     70
     71
                   (D) OTHER INFORMATION: N equals Inosine
            (ix) FEATURE:
     73
     74
                   (A) NAME/KEY: modified base
     75
                   (B) LOCATION: 18
     76
                   (D) OTHER INFORMATION: N equals Inosine
     78
            (ix) FEATURE:
                   (A) NAME/KEY: modified base
     79
     80
                   (B) LOCATION: 21
     81
                   (D) OTHER INFORMATION: N equals Inosine
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            (ix) FEATURE:
     85
                   (A) NAME/KEY: modified base
                   (B) LOCATION: 24
     86
     87
                   (D) OTHER INFORMATION: N equals Inosine
     90
            (ix) FEATURE:
     91
                   (A) NAME/KEY: modified base
     92
                   (B) LOCATION: 27
     93
                   (D) OTHER INFORMATION: N equals Inosine
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
     95
     97 ACAGAATTCT GGGTNGTNAC NGCNGCNCAY TG
     100 (2) INFORMATION FOR SEQ ID NO: 2:
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              (i) SEQUENCE CHARACTERISTICS:
     103
                    (A) LENGTH: 29 base pairs
     104
                    (B) TYPE: nucleic acid
     105
                    (C) STRANDEDNESS: single
     106
                    (D) TOPOLOGY: linear
             (ii) MOLECULE TYPE: DNA
W--> 108
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     110
     111
                    (A) NAME/KEY: modified base
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                    (B) LOCATION: 12
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                    (D) OTHER INFORMATION: N equals Inosine
     115
             (ix) FEATURE:
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                    (A) NAME/KEY: modified base
     117
                    (B) LOCATION: 15
     118
                    (D) OTHER INFORMATION: N equals Inosine
     120
             (ix) FEATURE:
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                    (A) NAME/KEY: modified base
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                    (B) LOCATION: 18
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                    (D) OTHER INFORMATION: N equals Inosine
     125
             (ix) FEATURE:
     126
                    (A) NAME/KEY: modified base
     127
                    (B) LOCATION: 21
     128
                    (D) OTHER INFORMATION: N equals Inosine
     130
             (ix) FEATURE:
```

(A) NAME/KEY: modified base

131

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/040,647

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	132	, ,																	
	133																		
	135	37 ACAGAATTCA RNGGNCCNCC NSWRTCNCC 40 (2) INFORMATION FOR SEQ ID NO: 3: 42 (i) SEQUENCE CHARACTERISTICS:															20		
																	29		
	142																		
	143			•	•					-	rs								
	144																		
	145	(D) TOPOLOGY: linear																	
	146																		
W>																			
	151																		
	152	, , , , , , , , , , , , , , , , , , ,																	
	154		/vi) SE(•					SEO :	וא חו	7 · 3							
		CCCC	•		_									יה כי	rc co	CG C	rg	4	9
	157	CGC	Joon	JAG (ייייייייייייייייייייייייייייייייייייייי											la Le		•	
	158						1	-1	-u	-9 0.	5		-u -			LO			
		CTG	CTG	GCT	CGG	GCT		CTC	AGG	AAG	CCG	GAG	TCG	CAG	-	GCG	GCG	9	7
																Ala			
	162				15		4		,	20					25				
		CCG	TTA	TCA	GGA	CCA	TGC	GGC	CGA	CGG	GTC	ATC	ACG	TCG	CGC	ATC	GTG	14	5
																Ile			
	166			30	_		_	-	35	_				40	_				
	168	GGT	GGA	GAG	GAC	GCC	GAA	CTC	GGG	CGT	TGG	CCG	TGG	CAG	GGG	AGC	CTG	19	3
	169	Gly	Gly	Glu	Asp	Ala	Glu	Leu	Gly	Arg	Trp	Pro	Trp	Gln	Gly	Ser	Leu		
	170		45					50					55						
																CAC		24	1
	173	Arg	Leu	Trp	Asp	Ser	His	Val	Cys	Gly	Val	Ser	Leu	Leu	Ser	His	Arg		
	174	60					65					70					75		
																GAT		28	9
		\mathtt{Trp}	Ala	Leu	Thr		Ala	His	Cys	Phe		Thr	Asp	Leu	Ser	Asp	Pro		
	178					80					85					90			_
																TCC		33	/
		Ser	GLY	Trp		Val	GIn	Phe	GLY		Leu	Thr	ser	Met		Ser	Pne		
	182	maa		ama.	95		m. a			100	ma a	mma	am.	таа	105	* 111.0	m » m	20	_
																ATC		38)
		тгр	ser		GIII	Ala	TAL	TYL		Arg	TYL	Pne	Val		ASII	Ile	TYL		
	186	CTC	A C C	110	CCC	መልሮ	CTC	CCC	115	መረገአ	CCC	תי א תי	CAC	120	CCC	TTG	GT/G	43	3
																Leu		40	,
	189	neu	125	PIO	Arg	тут	цец	130	ASII	261	PIO	TÄT	135	116	AIG	пеп	Val		
		ΔAG		ጥርጥ	GCA	ССТ	CTC		TAC	ΔСТ	ΔΔΔ	CAC		CAG	CCC	ATC	тст	48	1
																Ile		10.	-
	193	-	LCu	201		0	145		-1-	****	-10	150					155		
			CAG	GCC	TCC	ACA		GAG	ттт	GAG	AAC		ACA	GAC	TGC	TGG		52	9
																Trp		- -	
	197					160					165			E	- 4 -	170	. –		
		ACT	GGC	TGG	GGG		ATC	AAA	GAG	GAT		GCA	CTG	CCA	TCT	CCC	CAC	57	7

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200	Thr	Gly	Trp	Gly	Tyr	Ile	Lys	Glu	Asp	Glu	Ala	Leu	Pro	Ser	Pro	His	
201				175					180					185			
												AAC					625
	Thr	Leu		Glu	Val	Gln	Val		Ile	Ile	Asn	Asn		Met	Cys	Asn	
205		a= a	190			a		195	000		a. a	3.00	200	003	G 3 G	a m.c	672
												ATC					673
	HIS		Pne	Leu	гĀг	туг	210	Pne	Arg	ьуѕ	ASP	Ile 215	Pile	СТА	ASP	Met	
209	CTT	205	CCT	ccc	አአጥ	GCC		GGC	GGG	ΔAG	СΔТ	GCC	тсс	ጥጥር	GGT	GAC	721
												Ala					, 21
	220	Cys	mu	OI,	21011	225	0111				230		0,2		011	235	
		GGT	GGA	CCC	TTG		TGT	AAC	AAG	GAT		CTG	TGG	TAT	CAG	ATT	769
												Leu					
217		_	•		240		-		-	245	-		_	-	250		
219	GGA	GTC	GTG	AGC	TGG	GGA	GTG	GGC	TGT	GGT	CGG	CCC	AAT	CGG	CCC	GGT	817
220	Gly	Val	Val	Ser	Trp	Gly	Val	Gly	Cys	Gly	Arg	Pro	Asn	Arg	Pro	Gly	
221				255					260					265			
												ATC					865
	Val	Tyr		Asn	Ile	Ser	His		Phe	Glu	Trp	Ile		Lys	Leu	Met	
225			270					275					280				012
												TGG					913
	Ala		Ser	GLY	Met	Ser		Pro	Asp	Pro	ser	Trp	Pro	Leu	Leu	Pne	
228	mma	285	amm.	OM C	maa	COM	290	CCA	CITIC	CEC	ccc	295	CTC	ጥር እ			955
												CCG Pro					933
		PIO	ьeu	ьeu	пъ		ried	PIU	пец	neu	GIY	FIO	Val				
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234	GCC					AG CO					AGTC					TTCTGT AAAAA	1015 1075
234 236	GCC	GTTT(GGT A	ATA	AACA	AG CO					AGTC					TTCTGT AAAAAA	
234 236 238	GCC!	GTTT(AAAA	GGT A	ATAA AAAA	AAAA AAAA	AG CO CA T'	rccao	GTTG <i>l</i>	A TGC		AGTC						1075
234 236 238	GCC! CTT(AAAA	GTTT(AAAA INF(GGT A	AAAAA AAAAA TION	AACA(AAAA/ FOR	AG CO CA T A SEQ	ICCA(GTTG/	A TGO		AGTC						1075
234 236 238 241	GCCTTC AAAA (2)	GTTT(AAAA INF(GGT A AAA A ORMA) SE(AATAA AAAAA TION QUENG	AACAC AAAAA FOR CE CI	AG CO CA T' A SEQ HARAO	ICCA(GTTGA NO: 4	A TGO A: CS:	CCTT	AGTC						1075
234 236 238 241 243 244 245	GCCTC CTTC AAAA (2)	GTTT(AAAA INF(GGT A AAA A ORMAT) SE((1	AATAA AAAAA TION UEN(A) LI (3) TY	AACAC AAAAA FOR CE CH ENGTH (PE:	AG CO CA TO A SEQ HARAC H: 30 amin	ICCAC ID 1 CTERI 12 ar	GTTGA NO: 4 ISTIC mino cid	A TGO A: CS:	CCTT	AGTC						1075
234 236 238 241 243 244 245 246	GCCTCAAAAA	GTTT(AAAA INF((i)	GGT AAAA AORMAS OR	AATAAAAAAITION QUENG A) LI B) TY	AACACAAAAAAAACE CE CH ENGTH CPE:	AG CO CA TO A SEQ HARAC H: 30 amin	ICCAC ID 1 CTER: 12 ar no ac line	NO: 4 ISTIC mino cid ear	A TGO A: CS:	CCTT	AGTC						1075
234 236 238 241 243 244 245 246 248	GCCTCAAAAA	GTTT(AAAA) INF((i)	GGT AAA AORMAS ORMAS ORMAS ORMAS ORMAS (1)	AATAA TION QUENC A) LI B) TO	AACAC AAAAA FOR CE CH ENGTH (PE: OPOLC LE TY	AG CO CA TO A SEQ HARACH: 30 amin OGY:	ICCAC ID N CTERI 12 an no ac line prot	NO: 4 ISTIC mino cid ear tein	A TGO I: CS: acio	CCTT(AGTC GCAG	GGC					1075
234 236 238 241 243 244 245 246 248 250	GCCT CTTC AAAA (2)	GTTT(AAAA) INF((i;	GGT AAAA AORMAC OR	AATAA AAAAA FION QUENC A) LI B) TY D) TC LECUI	AACACAAAAAAACE CH FOR CE CH ENGTH CPE: DPOLC LE TY	AG CO CA TO A SEQ HARAO H: 30 amin OGY: VPE:	ICCAC ID N CTER: 12 ar no ac line prot	NO: 4 ISTIC nino cid ear tein	A TGO I: CS: acid	CCTTO	AGTC GCAG	GGC <i>i</i>	\TTT:	PTC A	AAAA	AAAAA	1075
234 236 238 241 243 244 245 246 248 250 252	GCCTCAAAA(2)	GTTT(AAAA) INF((i;	GGT AAAA AORMAC OR	AATAA AAAAA FION QUENC A) LI B) TY D) TC LECUI	AACACAAAAAAACE CH CE CH ENGTH (PE: DPOLC LE TY CE DH Gly	AG CO CA TO A SEQ HARAO H: 30 amin OGY: VPE:	ICCAC ID N CTER: 12 ar no ac line prot	NO: 4 ISTIC nino cid ear tein	A TGO I: CS: acid	ds Is ID NO Ala	AGTC GCAG	GGC	\TTT:	PTC A	AAAA <i>l</i> Arg	AAAAA	1075
234 236 238 241 243 244 245 246 248 250 252 253	GCCTCAAAA(2) Met	GTTT(AAAAA INF((ii (ii (xi)	GGT AAAA AORMAA ORMAA) SEG (A (I) MOI) SEG Ala	AATAA AAAAA FION QUENC A) LI B) TY D) TC LECUI QUENC Arg	AACAC FOR CE CH ENGTH (PE: DPOLC LE TY CE DH Gly 5	AG CO CA TO A SEQ HARAO H: 30 amin OGY: VPE: ESCRO	ID NOTER: 12 are no accomproduced produced produ	NO: 4 ISTIC mino cid ear tein DN: 5 Leu	A TGO I: CS: acio SEQ I	ds IS ID NO Ala 10	AGTC GCAG D: 4: Leu	GGC!	Leu	PTC A	Arg 15	AAAAAA	1075
234 236 238 241 243 244 245 246 250 252 253 255	GCCTCAAAA(2) Met	GTTT(AAAAA INF((ii (ii (xi)	GGT AAAA AORMAA ORMAA) SEG (A (I) MOI) SEG Ala	AATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	AACAC FOR CE CH ENGTH (PE: DPOLC LE TY CE DH Gly 5	AG CO CA TO A SEQ HARAO H: 30 amin OGY: VPE: ESCRO	ID NOTER: 12 are no accomproduced produced produ	NO: 4 ISTIC mino cid ear tein DN: 5 Leu	A TGG I: CS: acid SEQ I Leu Glu	ds IS ID NO Ala 10	AGTC GCAG D: 4: Leu	GGC <i>i</i>	Leu	Ala Ser	Arg 15	AAAAAA	1075
234 236 238 241 243 244 245 246 250 252 253 255 256	GCCC CTTC AAAA (2) Met 1 Gly	GTTTC AAAAA INFC (ii (ii (xi Gly Leu	GGT AAAA AORMAN ORMAN ORMAN ORMAN ORMAN (I (I (I) MOI ORMAN Arg	AATAA AAAAA FION QUENC A) LI B) TY D) TC LECUI QUENC Arg Lys 20	AACAC FOR CE CH ENGTH (PE: DPOLC LE TY CE DH Gly Pro	AG CO CA TO A SEQ HARACH: 30 amin OGY: VPE: ESCRI Ala	ID N CTER: 12 and acc line prot IPTIC Leu	NO: 4 ISTIC nino cid ear tein DN: 5 Leu Gln	A TGG I: CS: acid SEQ I Leu Glu 25	ds ID NO Ala 10 Ala	AGTC GCAG D: 4: Leu Ala	GGC!	Leu Leu	Ala Ser 30	Arg 15 Gly	Ala Pro	1075
234 236 238 241 243 244 245 246 252 253 255 256 258	GCCC CTTC AAAA (2) Met 1 Gly	GTTTC AAAAA INFC (ii (ii (xi Gly Leu	GGT AAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	AATAA AAAAA FION QUENC A) LI B) TY D) TC LECUI QUENC Arg Lys 20	AACAC FOR CE CH ENGTH (PE: DPOLC LE TY CE DH Gly Pro	AG CO CA TO A SEQ HARACH: 30 amin OGY: VPE: ESCRI Ala	ID N CTER: 12 and acc line prot IPTIC Leu	NO: 4 ISTIC mino cid ear tein DN: 5 Leu Gln Ser	A TGG I: CS: acid SEQ I Leu Glu 25	ds ID NO Ala 10 Ala	AGTC GCAG D: 4: Leu Ala	GGC!	Leu Leu Gly	Ala Ser 30	Arg 15 Gly	Ala Pro	1075
234 236 238 241 243 244 245 246 252 253 255 256 258 259	Met Gly	GTTTC AAAAA INFC (ii (xi) Gly Leu Gly	GGT AAAA AORMAS ORMAS ORMAS ORMAS ORMAS (I (I) MOI) SEG Ala Arg Arg 35	AATAA AAAAA FION QUENC A) LI B) TO CLECUI QUENC Arg Lys 20 Arg	AACAC AAAAA FOR CE CE ENGTE (PE: DPOLC LE TY CE DE Gly 5 Pro	AG CO CA TO A SEQ HARACH: 30 amin OGY: VPE: ESCRO Ala Glu	ID N CTER: 12 and accomprode 1ine prod IPTIC Leu Ser	NO: 4 ISTIC mino cid ear tein ON: 5 Leu Gln Ser 40	A TGO I: CS: acio EEQ Leu Glu 25 Arg	ID NO Ala 10 Ala Ile	AGTC GCAG D: 4: Leu Ala Val	GGCA Leu Pro	Leu Leu Gly 45	Ala Ser 30 Glu	Arg 15 Gly Asp	Ala Pro Ala	1075
234 236 241 243 244 245 246 252 253 255 256 258 259 261	Met Gly	GTTTC AAAAA INFC (ii (xi) Gly Leu Gly	GGT AAAA AORMAS ORMAS ORMAS ORMAS ORMAS (I (I) MOI) SEG Ala Arg Arg 35	AATAA AAAAA FION QUENC A) LI B) TO CLECUI QUENC Arg Lys 20 Arg	AACAC AAAAA FOR CE CE ENGTE (PE: DPOLC LE TY CE DE Gly 5 Pro	AG CO CA TO A SEQ HARACH: 30 amin OGY: VPE: ESCRO Ala Glu	ID N CTER: 12 and acc line prod IPTIC Leu Ser	NO: 4 ISTIC mino cid ear tein ON: 5 Leu Gln Ser 40	A TGO I: CS: acio EEQ Leu Glu 25 Arg	ID NO Ala 10 Ala Ile	AGTC GCAG D: 4: Leu Ala Val	GGC!	Leu Leu Gly 45	Ala Ser 30 Glu	Arg 15 Gly Asp	Ala Pro Ala	1075
234 236 241 243 244 245 246 252 253 255 256 258 259 261 262	Met 1 Gly Cys Glu	CATTTO AAAAA INFO (ii (xi Gly Leu Gly Leu 50	GGT AAAA AAAAA AAAAAAAAAAAAAAAAAAAAAAAA	AATAA AAAAA FION QUENC A) LI B) TY D) TC LECUI QUENC Arg Lys 20 Arg	AACAC AAAAA FOR CE CE ENGTE (PE: DPOLC LE TY CE DE Gly 5 Pro Val	AG CO CA TO A SEQ HARACH: 30 amin OGY: VPE: ESCRI Ala Glu Ile	ID NOTER: 12 are no accomprosed prosed prose	NO: 4 ISTIC mino cid ear tein ON: 5 Leu Gln Ser 40 Gln	A TGG I: CS: acid GEQ Leu Glu 25 Arg Gly	ds ID NO Ala 10 Ala Ile Ser	AGTC GCAG D: 4: Leu Ala Val Leu	GGCA Leu Pro Gly Arg	Leu Leu Gly 45 Leu	Ala Ser 30 Glu Trp	Arg 15 Gly Asp	Ala Pro Ala Ser	1075
234 236 241 243 244 245 246 252 253 255 256 258 259 261 262 264 265	Met 1 Gly Cys Glu His 65	CATTTO AAAAA INFO (ii (xi Gly Leu Gly Leu 50 Val	GGT AAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	AATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	AACAC AAAAA FOR CE CH C	AG CO CA TTA SEQ HARACH: 35 amin OGY: VPE: ESCRI Ala Glu Ile Pro Ser 70	ID NOTER: 12 are no accomprosed prosed prose	NO: 4 ISTIC mino cid ear tein ON: 5 Leu Gln Ser 40 Gln Leu	SEQ Deu Constant Cons	ds ID NO Ala 10 Ala Ile Ser His	AGTC GCAG D: 4: Leu Ala Val Leu Arg 75	GGCA Leu Pro Gly Arg 60	Leu Leu Gly 45 Leu Ala	Ala Ser 30 Glu Trp Leu	Arg 15 Gly Asp Asp	Ala Pro Ala Ser Ala 80	1075
234 236 241 243 244 245 246 252 253 255 256 258 259 261 262 264 265	Met 1 Gly Cys Glu His 65	CATTTO AAAAA INFO (ii (xi Gly Leu Gly Leu 50 Val	GGT AAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	AATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	AACAC AAAAA FOR CE CH C	AG CO CA TTA SEQ HARACH: 35 amin OGY: VPE: ESCRI Ala Glu Ile Pro Ser 70	ID NOTER: 12 are no accomprosed prosed prose	NO: 4 ISTIC mino cid ear tein ON: 5 Leu Gln Ser 40 Gln Leu	SEQ Deu Constant Cons	ds ID NO Ala 10 Ala Ile Ser His	AGTC GCAG D: 4: Leu Ala Val Leu Arg 75	GGCA Leu Pro Gly Arg 60	Leu Leu Gly 45 Leu Ala	Ala Ser 30 Glu Trp Leu	Arg 15 Gly Asp Asp Thr	Ala Pro Ala Ser Ala 80	1075
234 238 241 243 244 245 246 252 253 255 256 258 261 262 264 265 267 268	Met 1 Gly Cys Glu His 65 Ala	CATTTO AAAAA INFO (ii (xi (xi Gly Leu 50 Val His	GGT AAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	AATAA AAAAA FION QUENC A) LH B) TY C) TC LECUI QUENC Arg Lys 20 Arg Arg Gly Phe	AACAC AAAAA FOR CE CE ENGTH OPOLO EE TY CE DE Gly 5 Pro Val Trp Val Glu 85	AG CCA TO A SEQ HARACH: 30 amin DGY: CPE: ESCRUTALA Glu Ile Pro Ser 70 Thr	ID NOTES IN THE TENT IN THE TE	NO: 4 ISTIC mino cid ear tein DN: 5 Leu Gln Ser 40 Gln Leu Leu	A TGO I: CS: acio EEQ I Leu Glu 25 Arg Gly Ser Ser	ds ID NO Ala 10 Ala Ile Ser His Asp 90	O: 4: Leu Ala Val Leu Arg 75 Pro	GGCA Leu Pro Gly Arg 60	Leu Leu Gly 45 Leu Ala Gly	Ala Ser 30 Glu Trp Leu	Arg 15 Gly Asp Asp Thr Met 95	Ala Pro Ala Ser Ala 80 Val	1075

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	271				100					105					110			
	273	Tyr	Tyr	Thr	Arg	Tyr	Phe	Val	Ser	Asn	Ile	Tyr	Leu	Ser	Pro	Arg	\mathtt{Tyr}	
	274		_	115					120					125				
	276	Leu	Gly	Asn	Ser	Pro	Tyr	Asp	Ile	Ala	Leu	Val	Lys	Leu	Ser	Ala	Pro	
	277		130					135					140					
	279	Val	Thr	Tyr	Thr	Lys	His	Ile	Gln	Pro	Ile	Cys	Leu	Gln	Ala	Ser	Thr	
		145		•		-	150					155					160	
	282	Phe	Glu	Phe	Glu	Asn	Arq	Thr	Asp	Cys	Trp	Val	Thr	Gly	Trp	Gly	Tyr	
	283					165	_		•	-	170			_	-	175	_	
		Ile	Lvs	Glu	Asp		Ala	Leu	Pro	Ser	Pro	His	Thr	Leu	Gln	Glu	Val	
	286		-1-		180					185					190			
		Gln	Va 1	Δla		Tle	Asn	Asn	Ser		Cvs	Asn	His	Leu	Phe	Leu	Lvs	
	289	0111	, 41	195	110				200		0,70			205			-1-	
		ጥኒኒዮ	Sar		Δra	T.vc	Δen	Tle		Glv	Asn	Met	Va 1		Δla	Gly	Asn	
	292	ı yı	210	riie	пту	цуз	пор	215	1110	O.L.J	110P	1100	220	0,5		0-1	11011	
		λla		C117	C1++	Twa	λcn		Cvc	Dho	Clv	λen		Glv	Glv	Pro	Len	
			GIII	СТА	СТУ	гуѕ		нта	СуЗ	Pile	GLY	235	Ser	СТУ	СТУ	FIO	240	
		225	a	3	T		230	T	m	m	01 m		a1	1701	17.5.1	Cor		
		Ата	Cys	Asn	гĀЗ		GIY	ьeu	тгр	Tyr		116	СТА	Val	Val	Ser	пр	
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	342	Gly	Gly	Glu	Asp	Ala	Glu	Leu	Gly	Arg	\mathtt{Trp}	Pro	Trp	Gln	Gly	Ser	Leu	

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VERIFICATION SUMMARY

DATE: 05/07/2002 TIME: 11:16:48 PATENT APPLICATION: US/10/040,647

Input Set : N:\Crf3\RULE60\10040647.raw Output Set: N:\CRF3\05072002\J040647.raw

L:26 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:] L:27 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:] L:66 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1 L:108 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=2 L:148 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3 L:321 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5 L:406 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5 L:495 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7 L:641 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9 L:928 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11 L:944 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=12 L:959 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=13 L:973 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=14 L:1030 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=18 L:1043 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=19 L:1057 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=20 L:1071 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=21 L:1085 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=22 L:1099 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=23 L:1128 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25 L:1287 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27 L:1430 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=28 L:1483 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=29 L:1527 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=30